What is claimed is:

1. DNA comprising an open reading frame encoding a protein characterized by an amino acid sequence comprising a component sequence of at least 150 amino acid residues having 40% or more identity with an aligned component sequence of SEQ ID NO: 3.

2. The DNA according to claim 1 comprising an open reading frame encoding a protein having the formula R_1-R_2-R_3, wherein
   - R_1, R_2 and R_3 constitute component sequences consisting of amino acid residues independently selected from the group of the amino acid residues Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, and His,
   - R_1 and R_3 consist independently of 0 to 3000 amino acid residues;
   - R_2 consists of at least 150 amino acid residues; and
   - R_2 is at least 40% identical to an aligned component sequence of SEQ ID NO: 3.

3. The DNA according to claim 1 comprising an open reading frame encoding one or more SWI2/SNF2-like ATPase/helicase motifs.

4. The DNA according to claim 1 comprising an open reading frame encoding a protein having a component sequence defined by amino acids 478-490, 584-600, 617-630, 654-668, 676-690, 718-734, 776-788, 1222-1233, 1738-1749 or 1761-1770 of SEQ ID NO: 3.

5. The DNA according to claim 1, wherein the open reading frame encodes a protein characterized by the amino acid sequence of SEQ ID NO: 3, an allelic amino acid sequence having amino acid residue K instead of M at position 705 of SEQ ID NO: 3, or an amino acid residue D instead of E at position 1219 of SEQ ID NO: 3.

6. The DNA according to claim 1 characterized by the nucleotide sequence of SEQ ID NO: 1 or SEQ ID NO: 2.

7. The DNA according to claim 1, wherein expression of RNA, complementary to mRNA transcribed therefrom, releases silencing of a transgenic marker gene.

8. The protein encoded by the open reading frame of any one of claims 1 to 7.

9. A method of producing DNA according to claim 1, comprising
   - screening a DNA library for clones which are capable of hybridizing to a fragment of the DNA defined by SEQ ID NO: 1 or SEQ ID NO: 2, wherein said fragment has a length of at least 15 nucleotides;
   - sequencing hybridizing clones;
   - purifying vector DNA of clones comprising an open reading frame encoding a protein characterized by an amino acid sequence comprising a component sequence of at least 150 amino acid residues having 40% or more sequence identity to SEQ ID NO: 3
   - optionally further processing the purified DNA.

10. A polymerase chain reaction wherein at least one oligonucleotide used comprises a sequence of nucleotides which represents 15 or more basepairs of SEQ ID NO: 1 or SEQ ID NO: 2.